compounds and/or natural products for antagonist or agonist activity within a short amount of time. Specific assays or tests include homogeneous assay formats such as fluorescence resonance energy transfer, time resolved fluorescence resonance energy transfer, fluorescence polarization, scintillation proximity assays, reporter gene assays, fluorescence quenched enzyme substrate, chromogenic enzyme substrate and electrochemiluminesence, as well as, more traditional heterogeneous assay formats such as enzyme linked immunosorbant assays (ELISA) or radioimmunoassays. Homogeneous assays are mix and read style assays that are very amenable to robotic application, whereas heterogeneous assays require separation of bound analyte from free analyte by more complex unit operations such as filtration, centrifugation or washing. These assays can be utilized to detect a wide variety of specific biomolecular interactions and the inhibition of specific biomolecular interactions by small organic molecules, drug candidates, antibodies, peptides and other antagonists and/or agonists. Specific biomolecular interactions include, but are not limited to, protein-protein interactions, receptor-ligand interactions, enzyme-substrate interactions, etc.

A1 cont.

On page 30, lines 9-21, please delete the embedded hyperlinks and edit the paragraph to read as follows:

A2

For example, chromosomes can be mapped by radiation hybridization. PCR is performed using the Whitehead Institute/MIT Center for Genome Research Genebridge4 panel of 93 radiation hybrids (at the Whitehead Institute/MIT web site "genome.wi.mit.edu/ftp/distribution/human_STS_releases/july97/rhmap/genebridge4.html"). Primers are used which lie within a putative exon of the gene of interest and which amplify a product from human genomic DNA, but do not amplify hamster genomic DNA. The results of the PCRs are converted into a data vector that is submitted to the Whitehead/MIT Radiation Mapping site on the internet ("seq.wi.mit.edu"). The data is scored and the chromosomal assignment and placement relative to known Sequence Tag Site (STS) markers on the radiation hybrid map is provided. The following web site provides additional information about radiation hybrid mapping: "genome.wi.mit.edu/ftp/distribution/human_STS_releases/july97/07-97.INTRO.html".